

SEQUENCE LISTING

<110> Brugliera, Filippa
Holton, Timothy A.
Michael, Michael Z.

<120> GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
AND USES THEREFOR

<130> 11658

<140> 09/142,108

<141> 1998-09-01

<150> PN8386

<151> 1996-03-01

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<170> PatentIn Ver. 2.1

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His Lys Ile Asn Ser Ser Asp Glu Thr Lys Gly His Ser Asp Leu Leu	
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Asn Met Leu Ile Ser Leu Lys Asp Ala Asp Asp Ala Glu Gly Gly Arg	
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Leu Thr Asp Val Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Ala Ala	
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Gly Thr Asp Thr Thr Ser Ser Thr Val Glu Trp Cys Ile Ala Glu Leu	
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Val Arg His Pro Glu Ile Leu Ala Gln Val Gln Lys Glu Leu Asp Ser	
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Gln	Gly	Val	Ile	Ala	Lys	Met	Lys	Lys	Leu	His	Leu	Arg	Phe	Asp	Ser			
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Thr	Lys	Gly	His	Ser	Asp	Leu	Leu	Asn	Met	Leu	Ile	Ser	Leu	Lys	Asp			
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Ala	His	Glu	Ser	Cys	Glu	Val	Asn	Gly	Tyr	Leu	Ile	Pro	Lys	Gly	Ser			
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 Asp Gly Gly Ser Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn
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 Met Phe Thr Ala Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp Ala
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 Ile Ala Glu Leu Ile Arg His Pro Asp Ile Met Val Lys Ala Gln Glu
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 Ile Ala Gln Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Asn Phe Arg
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 Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala Ser Glu Ser
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 Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Phe Asp
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 Gly His Met Gly Leu Gly Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu
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Leu His Ala Asn Val Ala His Lys His Leu Ile Gly Asn Phe Ser Trp			
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Arg Ser Tyr Ala Gly Gln Pro Glu Tyr Arg Arg Lys Ser Leu Leu Gly			
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Phe Thr Leu Gln Arg Ala Val Pro Ser Val Val His Pro Lys Pro Arg			
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Ala Ser Trp Thr Arg Tyr Met Ala Cys Thr Lys Leu Thr Phe			
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 Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser Asp
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 Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala Ser Glu Ser
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 Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Phe Asp
 115 120 125
 Gly His Met Gly Leu Gly Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu
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tgacaatggt agggctcatt gcaactatgc agtcaatagc ttcttccaaa agaaagggtca	5237
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gttttcagaa tggttaacact cttgtgatct ttagaaccct aaaaaatttt gagtctcaga	5357
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agaactttga aggataccat tttatttttt ttggacaaag aaggatagcc atttaatact	5597
acactttaat gttggattaa ctaacttatt atgcctattt aatggcctac actttaagtg	5657
gacacaagct tgatttggtt ataaaaaaag tgcactataa tcttatttta ctgaaccctt	5717
ttttctatga tttttttact aaactttaga taacatctac aacaattcaa ttgccttttt	5777
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aacggttctt tgaaaacaca ttaatgataa ataaattgaa aagtatagag atggcaattg	5897
tttcaaaagc taatctttct gcttgctaact actttacata aaaaacaaaa aattaagaag	5957
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aagataaacg caagcaatac aattaggctt aattaagatt acgaatattg ttgtttgttt	6137
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gaagcaacag catcaccaca tttcccggcg gaaacagtcc atacactggc acaccatcca	6257
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aaaaaaatat gttatttata tgttcttggt gttttagaga taatttaatc tggatttcgg	6497
ttctttttta ctttccggtt ttaagaaaac aattatcaat gtaaaaacaa atctactatc	6557
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20 25 30

Leu Pro Pro Gly Pro Asn Pro Trp Pro Ile Ile Gly Asn Leu Pro His
35 40 45

Met Gly Thr Lys Pro His Arg Thr Leu Ser Ala Met Val Thr Thr Tyr
50 55 60

Gly Pro Ile Leu His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala
65 70 75 80

Ala Ser Lys Ser Val Ala Glu Gln Phe Leu Lys Ile His Asp Ala Asn
85 90 95

Phe Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala Tyr Asn
100 105 110

Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly His Arg Trp Arg Leu Leu
115 120 125

Arg Lys Ile Ser Ser Val His Leu Phe Ser Ala Lys Ala Leu Glu Asp
130 135 140

Phe Lys His Val Arg Gln
145 150

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<211> 147

<212> PRT

<213> Arabidopsis thaliana

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Pro Val Asn Leu Gly Gln Leu Val Asn Met Cys Val Val Asn Ala Leu
20 25 30

Gly Arg Glu Met Ile Gly Arg Arg Leu Phe Gly Ala Asp Ala Asp His
35 40 45

Lys Ala Asp Glu Phe Arg Ser Met Val Thr Glu Met Met Ala Leu Ala
50 55 60

Gly Val Phe Asn Ile Gly Asp Phe Val Pro Ser Leu Asp Trp Leu Asp
65 70 75 80

Leu Gln Gly Val Ala Gly Lys Met Lys Arg Leu His Lys Arg Phe Asp
85 90 95

Ala Phe Leu Ser Ser Ile Leu Lys Glu His Glu Met Asn Gly Gln Asp

100 105 110

Gln Lys His Thr Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly Thr
115 120 125

Asp Leu Asp Gly Asp Gly Gly Ser Leu Thr Asp Thr Glu Ile Lys Ala
130 135 140

Leu Leu Leu
145

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Glu Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser
35 40 45

Asp Ile Ala Gln Leu Pro Tyr Leu Gln
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<212> PRT
<213> Arabidopsis thaliana

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Pro Lys Gly Ser Thr Leu Leu Thr Asn Ile Trp Ala Ile Ala Arg Asp
35 40 45

Pro Asp Gln Trp Ser Asp Pro Leu Ala Phe Lys Pro Glu Arg Phe Leu
50 55 60

Pro Gly Gly Glu Lys Ser Gly Val Asp Val Lys Gly Ser Asp Phe Glu
65 70 75 80

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Leu
85 90 95

Gly Leu Arg Thr Ile Gln Phe Leu Thr Ala Thr Leu Val Gln Gly Phe
100 105 110

Asp Trp Glu Leu Ala Gly Gly Val Thr Pro Glu Lys Leu Asn Met Glu
115 120 125

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130 135 140

Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser Gly
145 150 155

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<213> Rosa hybrida

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Phe Ala Val Phe Leu Phe Arg Leu Leu Phe Ser Gly Lys Ser Gln Arg 25
15 20

cac tcg ctc cct ctc cct cct ggc ccc aaa cca tgg ccg gtg gtt ggc 147
His Ser Leu Pro Leu Pro Pro Gly Pro Lys Pro Trp Pro Val Val Gly 40
30 35

aac tta cct cac ttg ggc ccc ttc ccg cac cac tcc atc gcg gag ttg 195
Asn Leu Pro His Leu Gly Pro Phe Pro His His Ser Ile Ala Glu Leu 55
45 50

gcg aag aaa cac ggg ccg ctc atg cac ctc cgc ctc ggc tac gtt gac 243
Ala Lys Lys His Gly Pro Leu Met His Leu Arg Leu Gly Tyr Val Asp 70
60 65

gtā gtc gtg gcg gca tca gca tcc gta gcg gcc cag ttc ttg aag act 291
Val Val Val Ala Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr 90
75 80 85

cac gac gcc aat ttc tcc agc cga ccg ccc aac tcc ggc gcc aag cac 339
His Asp Ala Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His 105
95 100

ctc gcc tat aac tac cag gac ctc gtg ttc agg ccg tac ggt cca cgg 387
Leu Ala Tyr Asn Tyr Gln Asp Leu Val Phe Arg Pro Tyr Gly Pro Arg 120
110 115

tgg cgc atg ttc cgg aag atc agc tcc gtc cat ctg ttc tcc ggc aaa 435
Trp Arg Met Phe Arg Lys Ile Ser Ser Val His Leu Phe Ser Gly Lys 135
125 130

gcc ttg gat gat ctt aaa cac gtc cgg cag gag gag gta agt gtg cta	483
Ala Leu Asp Asp Leu Lys His Val Arg Gln Glu Glu Val Ser Val Leu	
140 145 150	
gcg cat gcc ttg gca aat tca ggg tca aag gta gtg aac ctg gcg caa	531
Ala His Ala Leu Ala Asn Ser Gly Ser Lys Val Val Asn Leu Ala Gln	
155 160 165 170	
ctg ctg aac ctg tgc acg gtc aat gct cta gga agg gtg atg gta ggg	579
Leu Leu Asn Leu Cys Thr Val Asn Ala Leu Gly Arg Val Met Val Gly	
175 180 185	
cgg agg gtt ttc ggc gac ggc agc gga ggc gac gat ccg aag gcg gac	627
Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Asp Asp Pro Lys Ala Asp	
190 195 200	
gag ttc aaa tcg atg gtg gtg gag atg atg gtg ttg gca gga gtg ttc	675
Glu Phe Lys Ser Met Val Val Glu Met Met Val Leu Ala Gly Val Phe	
205 210 215	
aac ata ggt gac ttc atc ccc tct ctc gaa tgg ctt gac ttg caa ggc	723
Asn Ile Gly Asp Phe Ile Pro Ser Leu Glu Trp Leu Asp Leu Gln Gly	
220 225 230	
gtg gcg tcc aag atg aag aag ctc cac aag aga ttc gac gac ttc ttg	771
Val Ala Ser Lys Met Lys Lys Leu His Lys Arg Phe Asp Asp Phe Leu	
235 240 245 250	
aca gcc att gtc gag gac cac aag aag ggc tcc ggc acg gcg ggg cac	819
Thr Ala Ile Val Glu Asp His Lys Lys Gly Ser Gly Thr Ala Gly His	
255 260 265	
gtc gac atg ttg acc act ctg ctc tcg ctc aag gaa gac gcc gac ggc	867
Val Asp Met Leu Thr Thr Leu Leu Ser Leu Lys Glu Asp Ala Asp Gly	
270 275 280	
gaa gga ggc aag ctc acc gat act gaa atc aaa gct ttg ctt ttg aac	915
Glu Gly Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn	
285 290 295	
atg ttc acg gct ggc act gat acg tca tcg agc acg gtg gaa tgg gca	963
Met Phe Thr Ala Gly Thr Asp Thr Ser Ser Thr Thr Val Glu Trp Ala	
300 305 310	
ata gct gaa ctc att cgg cac cct cat atg cta gcg cga gtt cag aaa	1011
Ile Ala Glu Leu Ile Arg His Pro His Met Leu Ala Arg Val Gln Lys	
315 320 325 330	
gag ctt gac gat ttt gtt ggc cat gac cga ctt gtg acc gaa tcc gac	1059
Glu Leu Asp Asp Phe Val Gly His Asp Arg Leu Val Thr Glu Ser Asp	
335 340 345	
ata ccc aac ctc cct tac ctc caa gcc gtg atc aag gaa acg ttc cga	1107
Ile Pro Asn Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Thr Phe Arg	
350 355 360	
ctc cac cca tcc act cct ctc tcg ttg cct cgt atg gca gcc gag agt	1155
Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Ala Ala Glu Ser	
365 370 375	

tgc gaa atc aac ggg tac cac atc ccg aaa ggc tcc aca ctc ttg gtc 1203
 Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Leu Val
 380 385 390

aat gta tgg gcc ata tgc cgt gac ccg gct gaa tgg gcc gac cca ctg 1251
 Asn Val Trp Ala Ile Ser Arg Asp Pro Ala Glu Trp Ala Asp Pro Leu
 395 400 405 410

gag ttc aag ccc gag agg ttc ctg ccg ggg ggc gaa aag cct aat gtt 1299
 Glu Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val
 415 420 425

gat att aga gga aac gat ttt gaa gtc ata ccc ttc ggt gcc ggg cga 1347
 Asp Ile Arg Gly Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg
 430 435 440

aga ata tgt gcc ggg atg agc ttg ggc ctg cgt atg gtc cat tta atg 1395
 Arg Ile Cys Ala Gly Met Ser Leu Gly Leu Arg Met Val His Leu Met
 445 450 455

act gca aca ttg gtc cac gca ttt aat tgg gcc ttg gct gat ggg ctg 1443
 Thr Ala Thr Leu Val His Ala Phe Asn Trp Ala Leu Ala Asp Gly Leu
 460 465 470

acc gct gag aag tta aac atg gat gaa gca tat ggg ctc act cta caa 1491
 Thr Ala Glu Lys Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln
 475 480 485 490

cga gct gca ccg tta atg gtg cac ccg cgc acc agg ctg gcc cca cag 1539
 Arg Ala Ala Pro Leu Met Val His Pro Arg Thr Arg Leu Ala Pro Gln
 495 500 505

gca tat aaa act tca tca tct taa ttagagagct atgttctggg tgtgcccggt 1593
 Ala Tyr Lys Thr Ser Ser Ser
 510

ttgatgtctc catgttttct atttaggttt aaatctgtaa gataagggtga ttctatgctg 1653

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<211> 513

<212> PRT

<213> Rosa hybrida

<400> 15

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 20 25 30
 Pro Gly Pro Lys Pro Trp Pro Val Val Gly Asn Leu Pro His Leu Gly
 35 40 45
 Pro Phe Pro His His Ser Ile Ala Glu Leu Ala Lys Lys His Gly Pro
 50 55 60
 Leu Met His Leu Arg Leu Gly Tyr Val Asp Val Val Val Ala Ala Ser

65					70					75					80
Ala	Ser	Val	Ala	Ala	Gln	Phe	Leu	Lys	Thr	His	Asp	Ala	Asn	Phe	Ser
				85					90					95	
Ser	Arg	Pro	Pro	Asn	Ser	Gly	Ala	Lys	His	Leu	Ala	Tyr	Asn	Tyr	Gln
			100					105					110		
Asp	Leu	Val	Phe	Arg	Pro	Tyr	Gly	Pro	Arg	Trp	Arg	Met	Phe	Arg	Lys
		115					120					125			
Ile	Ser	Ser	Val	His	Leu	Phe	Ser	Gly	Lys	Ala	Leu	Asp	Asp	Leu	Lys
	130					135					140				
His	Val	Arg	Gln	Glu	Glu	Val	Ser	Val	Leu	Ala	His	Ala	Leu	Ala	Asn
145					150					155					160
Ser	Gly	Ser	Lys	Val	Asn	Leu	Ala	Gln	Leu	Leu	Asn	Leu	Cys	Thr	
			165					170					175		
Val	Asn	Ala	Leu	Gly	Arg	Val	Met	Val	Gly	Arg	Arg	Val	Phe	Gly	Asp
		180					185						190		
Gly	Ser	Gly	Gly	Asp	Asp	Pro	Lys	Ala	Asp	Glu	Phe	Lys	Ser	Met	Val
	195					200						205			
Val	Glu	Met	Met	Val	Leu	Ala	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Ile
	210					215					220				
Pro	Ser	Leu	Glu	Trp	Leu	Asp	Leu	Gln	Gly	Val	Ala	Ser	Lys	Met	Lys
225					230					235					240
Lys	Leu	His	Lys	Arg	Phe	Asp	Asp	Phe	Leu	Thr	Ala	Ile	Val	Glu	Asp
			245					250						255	
His	Lys	Lys	Gly	Ser	Gly	Thr	Ala	Gly	His	Val	Asp	Met	Leu	Thr	Thr
		260				265						270			
Leu	Leu	Ser	Leu	Lys	Glu	Asp	Ala	Asp	Gly	Glu	Gly	Gly	Lys	Leu	Thr
	275					280					285				
Asp	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn	Met	Phe	Thr	Ala	Gly	Thr
	290				295					300					
Asp	Thr	Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala	Ile	Ala	Glu	Leu	Ile	Arg
305					310					315					320
His	Pro	His	Met	Leu	Ala	Arg	Val	Gln	Lys	Glu	Leu	Asp	Asp	Phe	Val
			325					330						335	
Gly	His	Asp	Arg	Leu	Val	Thr	Glu	Ser	Asp	Ile	Pro	Asn	Leu	Pro	Tyr
		340					345					350			
Leu	Gln	Ala	Val	Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro
	355					360					365				
Leu	Ser	Leu	Pro	Arg	Met	Ala	Ala	Glu	Ser	Cys	Glu	Ile	Asn	Gly	Tyr
	370				375					380					
His	Ile	Pro	Lys	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ser
385					390					395					400
Arg	Asp	Pro	Ala	Glu	Trp	Ala	Asp	Pro	Leu	Glu	Phe	Lys	Pro	Glu	Arg
			405					410					415		
Phe	Leu	Pro	Gly	Gly	Glu	Lys	Pro	Asn	Val	Asp	Ile	Arg	Gly	Asn	Asp
		420					425					430			
Phe	Glu	Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Met
	435					440					445				
Ser	Leu	Gly	Leu	Arg	Met	Val	His	Leu	Met	Thr	Ala	Thr	Leu	Val	His
	450				455					460					
Ala	Phe	Asn	Trp	Ala	Leu	Ala	Asp	Gly	Leu	Thr	Ala	Glu	Lys	Leu	Asn
465					470					475					480
Met	Asp	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Ala	Pro	Leu	Met
			485					490					495		
Val	His	Pro	Arg	Thr	Arg	Leu	Ala	Pro	Gln	Ala	Tyr	Lys	Thr	Ser	Ser
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Ser

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 <213> Chrysanthemum

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 <222> (4)..(1530)

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Val Leu Tyr Val Phe Leu Asn Leu Ser Ser Arg Lys Ser Ala Arg Leu	
20 25 30	
cca ccc ggg cca aca cca tgg cct ata gtc ggg aac tta cca cac ctt	144
Pro Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu	
35 40 45	
ggc cca atc cca cac cac gca ctc gcg gcc tta gcc aag aag tac ggg	192
Gly Pro Ile Pro His His Ala Leu Ala Ala Leu Ala Lys Lys Tyr Gly	
50 55 60	
cca ttg atg cac ctg cgg ctc ggg tgt gtg gac gtg gtt gtg gcc gcg	240
Pro Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Val Ala Ala	
65 70 75	
tct gct tcc gta gct gca cag ttt tta aaa gtt cac gac gca aat ttt	288
Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe	
80 85 90 95	
gct agt agg ccg cca aat tct ggc gcg aaa cat gtg gcg tat aat tat	336
Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr	
100 105 110	
cag gat ctt gtg ttt gca cct tat ggt cca agg tgg cgt ttg tta agg	384
Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg	
115 120 125	
aag att tgt tcg gtc cat ttg ttt tct gct aaa gca ctt gat gat ttt	432
Lys Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe	
130 135 140	
cgt cat gtt cga cag gag gag gta gca gtc cta acc cgc gta cta ctg	480
Arg His Val Arg Gln Glu Glu Val Ala Val Leu Thr Arg Val Leu Leu	
145 150 155	
agt gct gga aac tca ccg gta cag ctt ggc caa cta ctt aac gtg tgt	528
Ser Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys	
160 165 170 175	
gcc aca aac gcc tta gca cgg gta atg tta ggt agg aga gtt ttc gga	576
Ala Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly	
180 185 190	
gac gga att gac agg tca gcc aat gag ttc aaa gat atg gta gta gag	624
Asp Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu	
195 200 205	

tta atg gta tta gca gga gaa ttt aac ctt ggt gac ttt att cct gta	672
Leu Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val	
210 215 220	
ctt gac cta ttc gac cta caa ggc att act aaa aaa atg aag aag ctt	720
Leu Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu	
225 230 235	
cat gtt cgg ttc gat tca ttt ctt agt aag atc gtt gag gag cat aaa	768
His Val Arg Phe Asp Ser Phe Leu Ser Lys Ile Val Glu Glu His Lys	
240 245 250 255	
acg gca cct ggt ggg ttg ggt cat act gat ttg ctg agc acg ttg att	816
Thr Ala Pro Gly Gly Leu Gly His Thr Asp Leu Leu Ser Thr Leu Ile	
260 265 270	
tca ctt aaa gat gat gct gat att gaa ggt ggg aag ctt aca gat act	864
Ser Leu Lys Asp Asp Ala Asp Ile Glu Gly Gly Lys Leu Thr Asp Thr	
275 280 285	
gaa atc aaa gct ttg ctt ctg aat tta ttc gct gcg gga aca gac aca	912
Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr	
290 295 300	
tcc tct agt aca gta gaa tgg gca ata gcc gaa ctc att cgt cat cca	960
Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg His Pro	
305 310 315	
caa ata tta aaa caa gcc cga gaa gag ata gac gct gta gtt ggt caa	1008
Gln Ile Leu Lys Gln Ala Arg Glu Glu Ile Asp Ala Val Val Gly Gln	
320 325 330 335	
gac cgg ctt gta aca gaa ttg gac ttg agc caa cta aca tac ctc cag	1056
Asp Arg Leu Val Thr Glu Leu Asp Leu Ser Gln Leu Thr Tyr Leu Gln	
340 345 350	
gct ctt gtg aaa gag gtg ttt agg ctc cac cct tca acg cca ctc tcc	1104
Ala Leu Val Lys Glu Val Phe Arg Leu His Pro Ser Thr Pro Leu Ser	
355 360 365	
tta cca aga ata tca tcc gag agt tgt gag gtc gat ggg tat tat atc	1152
Leu Pro Arg Ile Ser Ser Glu Ser Cys Glu Val Asp Gly Tyr Tyr Ile	
370 375 380	
cct aag gga tcc aca ctc ctc gtt aac gtg tgg gcc att gcg cga gac	1200
Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp	
385 390 395	
cca aaa atg tgg gcg gat cct ctt gaa ttt agg cct tct cgg ttt tta	1248
Pro Lys Met Trp Ala Asp Pro Leu Glu Phe Arg Pro Ser Arg Phe Leu	
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ccc ggg gga gaa aag ccc ggt gct gat gtt agg gga aat gat ttt gaa	1296
Pro Gly Gly Glu Lys Pro Gly Ala Asp Val Arg Gly Asn Asp Phe Glu	
420 425 430	
gtt ata cca ttt ggg gca gga cga agg att tgt gcg ggt atg agc cta	1344
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu	
435 440 445	

ggc ttg aga atg gtc cag ttg ctc att gca aca ttg gtc caa act ttt 1392
 Gly Leu Arg Met Val Gln Leu Leu Ile Ala Thr Leu Val Gln Thr Phe
 450 455 460

gat tgg gaa ctg gct aac ggg tta gag ccg gag atg ctc aac atg gaa 1440
 Asp Trp Glu Leu Ala Asn Gly Leu Glu Pro Glu Met Leu Asn Met Glu
 465 470 475

gaa gcg tat gga ttg acc ctt caa cgg gct gca ccc ttg atg gtt cac 1488
 Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val His
 480 485 490 495

ccg aag ccg agg tta gct ccc cac gta tat gaa agt att taa 1530
 Pro Lys Pro Arg Leu Ala Pro His Val Tyr Glu Ser Ile
 500 505

ggactagtttt ctcttttggcc tttttgtttc gcaaaggtta atgaataaac gatttcatga 1590

ctcagatagt tatgtaaaca attgtgtttg ctgtttatat atttatctat ttttctagaa 1650

caaaaaaaaaa 1660

<210> 17
 <211> 508
 <212> PRT
 <213> Chrysanthemum

<400> 17
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 Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu Gly
 35 40 45
 Pro Ile Pro His His Ala Leu Ala Ala Leu Ala Lys Lys Tyr Gly Pro
 50 55 60
 Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Val Ala Ala Ser
 65 70 75 80
 Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe Ala
 85 90 95
 Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr Gln
 100 105 110
 Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys
 115 120 125
 Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Arg
 130 135 140
 His Val Arg Gln Glu Glu Val Ala Val Leu Thr Arg Val Leu Leu Ser
 145 150 155 160
 Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys Ala
 165 170 175
 Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly Asp
 180 185 190
 Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu Leu
 195 200 205
 Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val Leu
 210 215 220
 Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu His
 225 230 235 240

Val	Arg	Phe	Asp	Ser	Phe	Leu	Ser	Lys	Ile	Val	Glu	Glu	His	Lys	Thr		
				245					250					255			
Ala	Pro	Gly	Gly	Leu	Gly	His	Thr	Asp	Leu	Leu	Ser	Thr	Leu	Ile	Ser		
			260					265					270				
Leu	Lys	Asp	Asp	Ala	Asp	Ile	Glu	Gly	Gly	Lys	Leu	Thr	Asp	Thr	Glu		
		275					280					285					
Ile	Lys	Ala	Leu	Leu	Leu	Asn	Leu	Phe	Ala	Ala	Gly	Thr	Asp	Thr	Ser		
	290					295					300						
Ser	Ser	Thr	Val	Glu	Trp	Ala	Ile	Ala	Glu	Leu	Ile	Arg	His	Pro	Gln		
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Ile	Leu	Lys	Gln	Ala	Arg	Glu	Glu	Ile	Asp	Ala	Val	Val	Gly	Gln	Asp		
			325						330					335			
Arg	Leu	Val	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Leu	Thr	Tyr	Leu	Gln	Ala		
			340					345					350				
Leu	Val	Lys	Glu	Val	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	Ser	Leu		
		355					360					365					
Pro	Arg	Ile	Ser	Ser	Glu	Ser	Cys	Glu	Val	Asp	Gly	Tyr	Tyr	Ile	Pro		
	370					375					380						
Lys	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp	Pro		
385					390					395					400		
Lys	Met	Trp	Ala	Asp	Pro	Leu	Glu	Phe	Arg	Pro	Ser	Arg	Phe	Leu	Pro		
			405						410					415			
Gly	Gly	Glu	Lys	Pro	Gly	Ala	Asp	Val	Arg	Gly	Asn	Asp	Phe	Glu	Val		
		420					425						430				
Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Met	Ser	Leu	Gly		
	435					440						445					
Leu	Arg	Met	Val	Gln	Leu	Leu	Ile	Ala	Thr	Leu	Val	Gln	Thr	Phe	Asp		
	450					455					460						
Trp	Glu	Leu	Ala	Asn	Gly	Leu	Glu	Pro	Glu	Met	Leu	Asn	Met	Glu	Glu		
465				470						475					480		
Ala	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Ala	Pro	Leu	Met	Val	His	Pro		
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Lys	Pro	Arg	Leu	Ala	Pro	His	Val	Tyr	Glu	Ser	Ile						
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 Met Ser Pro
 1
 tta gcc ttg atg atc ata agt acc tta tta ggg ttt ctc cta tac cac 163
 Leu Ala Leu Met Ile Ile Ser Thr Leu Leu Gly Phe Leu Leu Tyr His
 5 10 15
 tct ctt cgc tta cta ctc ttc tcc ggc caa ggt cgc cga cta cta cca 211

Ser	Leu	Arg	Leu	Leu	Leu	Phe	Ser	Gly	Gln	Gly	Arg	Arg	Leu	Leu	Pro		
20					25					30					35		
cca	ggt	cca	cgc	ccg	tgg	ccg	ctg	gtg	gga	aat	ctc	ccg	cac	tta	ggc	259	
Pro	Gly	Pro	Arg	Pro	Trp	Pro	Leu	Val	Gly	Asn	Leu	Pro	His	Leu	Gly		
				40					45					50			
ccg	aag	cca	cac	gcc	tcc	atg	gcc	gag	ctc	gcg	cga	gcc	tac	gga	ccc	307	
Pro	Lys	Pro	His	Ala	Ser	Met	Ala	Glu	Leu	Ala	Arg	Ala	Tyr	Gly	Pro		
			55					60					65				
ctc	atg	cac	cta	aag	atg	ggg	ttc	gtc	cac	gtc	gtg	gtg	gct	tcg	tcg	355	
Leu	Met	His	Leu	Lys	Met	Gly	Phe	Val	His	Val	Val	Val	Ala	Ser	Ser		
		70					75						80				
gcg	agc	gcg	gcg	gag	cag	tgc	ctg	agg	gtt	cac	gac	gcg	aat	ttc	ttg	403	
Ala	Ser	Ala	Ala	Glu	Gln	Cys	Leu	Arg	Val	His	Asp	Ala	Asn	Phe	Leu		
	85					90					95						
agc	agg	cca	ccc	aac	tcc	ggc	gcc	aag	cac	gtc	gct	tac	aac	tac	gag	451	
Ser	Arg	Pro	Pro	Asn	Ser	Gly	Ala	Lys	His	Val	Ala	Tyr	Asn	Tyr	Glu		
100					105					110					115		
gac	ttg	gtt	ttc	aga	ccg	tac	ggg	ccc	aag	tgg	agg	ctg	ttg	agg	aag	499	
Asp	Leu	Val	Phe	Arg	Pro	Tyr	Gly	Pro	Lys	Trp	Arg	Leu	Leu	Arg	Lys		
				120					125					130			
ata	tgc	gct	cag	cat	att	ttc	tcc	gtc	aag	gct	atg	gat	gac	ttc	agg	547	
Ile	Cys	Ala	Gln	His	Ile	Phe	Ser	Val	Lys	Ala	Met	Asp	Asp	Phe	Arg		
			135					140					145				
cgc	gtc	aga	gag	gaa	gag	gtg	gcc	atc	ctg	agt	cgc	gct	cta	gca	ggc	595	
Arg	Val	Arg	Glu	Glu	Glu	Val	Ala	Ile	Leu	Ser	Arg	Ala	Leu	Ala	Gly		
		150					155					160					
aaa	agg	gcc	gta	ccc	ata	ggc	caa	atg	ctc	aac	gtg	tgc	gcc	aca	aac	643	
Lys	Arg	Ala	Val	Pro	Ile	Gly	Gln	Met	Leu	Asn	Val	Cys	Ala	Thr	Asn		
	165					170					175						
gcc	cta	tct	cgc	gtc	atg	atg	ggg	cgg	cgc	gtg	gtg	ggc	cac	gcg	gat	691	
Ala	Leu	Ser	Arg	Val	Met	Met	Gly	Arg	Arg	Val	Val	Gly	His	Ala	Asp		
180					185					190					195		
gga	acc	aac	gac	gcc	aag	gcg	gag	gag	ttc	aaa	gcc	atg	gtc	gtc	gag	739	
Gly	Thr	Asn	Asp	Ala	Lys	Ala	Glu	Glu	Phe	Lys	Ala	Met	Val	Val	Glu		
				200					205					210			
ctc	atg	gtc	ctc	tcc	ggc	gtc	ttc	aac	atc	ggg	gat	ttc	atc	ccc	ttc	787	
Leu	Met	Val	Leu	Ser	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro	Phe		
			215					220					225				
ctc	gag	cct	ctc	gac	ttg	cag	gga	gtg	gct	tcc	aag	atg	aag	aaa	ctc	835	
Leu	Glu	Pro	Leu	Asp	Leu	Gln	Gly	Val	Ala	Ser	Lys	Met	Lys	Lys	Leu		
		230					235					240					
cac	gcg	cgg	ttc	gat	gca	ttc	ttg	acc	gag	att	gta	cga	gag	cgt	tgt	883	
His	Ala	Arg	Phe	Asp	Ala	Phe	Leu	Thr	Glu	Ile	Val	Arg	Glu	Arg	Cys		
	245					250					255						

cat ggg cag atc aac aac agt ggt gct cat cag gat gat ttg ctt agc	931
His Gly Gln Ile Asn Asn Ser Gly Ala His Gln Asp Asp Leu Leu Ser	
260 265 270 275	
acg ttg att tcg ttc aaa ggg ctt gac gat ggc gat ggt tcc agg ctc	979
Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly Ser Arg Leu	
280 285 290	
act gac aca gaa atc aag gcg ctg ctc ttg aac ctt ttg gac acg acg	1027
Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Leu Asp Thr Thr	
295 300 305	
tcg agc acg gtg gaa tgg gcc gta gcc gaa ctc cta cgc cac cct aag	1075
Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg His Pro Lys	
310 315 320	
aca tta gcc caa gtc cgg caa gag ctc gac tcg gtc gtg ggt aag aac	1123
Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val Gly Lys Asn	
325 330 335	
agg ctc gtg tcc gag acc gat ctg aat cag ctg ccc tat cta caa gct	1171
Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr Leu Gln Ala	
340 345 350 355	
gtc gtc aaa gaa act ttc cgc ctc cat cct ccg acg ccg ctc tct cta	1219
Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro Leu Ser Leu	
360 365 370	
ccg aga ctc gcg gaa gat gat tgc gag atc gac gga tac ctc atc ccc	1267
Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr Leu Ile Pro	
375 380 385	
aag ggc tcg acc ctt ctg gtg aac gtt tgg gcc ata gcc cgc gat ccc	1315
Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro	
390 395 400	
aag gtt tgg gcc gat ccg ttg gag ttt agg ccc gaa cga ttc ttg acg	1363
Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Leu Thr	
405 410 415	
ggc gga gaa aag gcc gac gtc gat gtc aag ggg aac gat ttc gaa gtg	1411
Gly Gly Glu Lys Ala Asp Val Asp Val Lys Gly Asn Asp Phe Glu Val	
420 425 430 435	
ata ccg ttc ggg gcg ggt cgt agg atc tgc gct ggc gtt ggc ttg gga	1459
Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Val Gly Leu Gly	
440 445 450	
ata cgt atg gtc caa ctg ttg acg gcg agt ttg atc cat gca ttc gat	1507
Ile Arg Met Val Gln Leu Leu Thr Ala Ser Leu Ile His Ala Phe Asp	
455 460 465	
ctg gac ctt gct aat ggg ctt ttg gcc caa aat ctg aac atg gaa gaa	1555
Leu Asp Leu Ala Asn Gly Leu Leu Ala Gln Asn Leu Asn Met Glu Glu	
470 475 480	
gca tat ggg ctt acg cta caa cgg gct gag cct ttg ttg gtc cac cct	1603
Ala Tyr Gly Leu Thr Leu Gln Arg Ala Glu Pro Leu Leu Val His Pro	
485 490 495	

agg ccg cgg ttg gcc act cat gtc tat taa ttaaattagg cctaaactac 1653
 Arg Pro Arg Leu Ala Thr His Val Tyr
 500 505

gatgaatgac ccatttaacg ttaataagag ttttcaattt atgtgagttt gcatgggtatg 1713

gtatgggtatg gtgcttgtaa taaattgtat ctggttaggtg tgttcattga tgataaatct 1773

agtttgtact gctgctcaaa aaaaaaaaaa aaaaaaaaaa aa 1815

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 Leu Tyr His Ser Leu Arg Leu Leu Leu Phe Ser Gly Gln Gly Arg Arg
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 Leu Leu Pro Pro Gly Pro Arg Pro Trp Pro Leu Val Gly Asn Leu Pro
 35 40 45
 His Leu Gly Pro Lys Pro His Ala Ser Met Ala Glu Leu Ala Arg Ala
 50 55 60
 Tyr Gly Pro Leu Met His Leu Lys Met Gly Phe Val His Val Val Val
 65 70 75 80
 Ala Ser Ser Ala Ser Ala Ala Glu Gln Cys Leu Arg Val His Asp Ala
 85 90 95
 Asn Phe Leu Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr
 100 105 110
 Asn Tyr Glu Asp Leu Val Phe Arg Pro Tyr Gly Pro Lys Trp Arg Leu
 115 120 125
 Leu Arg Lys Ile Cys Ala Gln His Ile Phe Ser Val Lys Ala Met Asp
 130 135 140
 Asp Phe Arg Arg Val Arg Glu Glu Glu Val Ala Ile Leu Ser Arg Ala
 145 150 155 160
 Leu Ala Gly Lys Arg Ala Val Pro Ile Gly Gln Met Leu Asn Val Cys
 165 170 175
 Ala Thr Asn Ala Leu Ser Arg Val Met Met Gly Arg Arg Val Val Gly
 180 185 190
 His Ala Asp Gly Thr Asn Asp Ala Lys Ala Glu Glu Phe Lys Ala Met
 195 200 205
 Val Val Glu Leu Met Val Leu Ser Gly Val Phe Asn Ile Gly Asp Phe
 210 215 220
 Ile Pro Phe Leu Glu Pro Leu Asp Leu Gln Gly Val Ala Ser Lys Met
 225 230 235 240
 Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Glu Ile Val Arg
 245 250 255
 Glu Arg Cys His Gly Gln Ile Asn Asn Ser Gly Ala His Gln Asp Asp
 260 265 270
 Leu Leu Ser Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly
 275 280 285
 Ser Arg Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Leu
 290 295 300
 Asp Thr Thr Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg
 305 310 315 320
 His Pro Lys Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val
 325 330 335

Gly Lys Asn Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr
 340 345 350
 Leu Gln Ala Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro
 355 360 365
 Leu Ser Leu Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr
 370 375 380
 Leu Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala
 385 390 395 400
 Arg Asp Pro Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg
 405 410 415
 Phe Leu Thr Gly Gly Glu Lys Ala Asp Val Asp Val Lys Gly Asn Asp
 420 425 430
 Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Val
 435 440 445
 Gly Leu Gly Ile Arg Met Val Gln Leu Leu Thr Ala Ser Leu Ile His
 450 455 460
 Ala Phe Asp Leu Asp Leu Ala Asn Gly Leu Leu Ala Gln Asn Leu Asn
 465 470 475 480
 Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Glu Pro Leu Leu
 485 490 495
 Val His Pro Arg Pro Arg Leu Ala Thr His Val Tyr
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 <212> DNA
 <213> Jap. Morning Glory

<220>
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 <222> (2)..(1555)

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 ttt ctt att ctc agg gtg aaa cag cgt tac cct tta cct ctc cca ccc 97
 Phe Leu Ile Leu Arg Val Lys Gln Arg Tyr Pro Leu Pro Leu Pro Pro
 20 25 30
 gga cca aaa cca tgg ccg gtg tta gga aac ctt ccc cac ctg ggc aag 145
 Gly Pro Lys Pro Trp Pro Val Leu Gly Asn Leu Pro His Leu Gly Lys
 35 40 45
 aag cct cac cag tcg att gcg gcc atg gct gag agg tac ggc ccc ctc 193
 Lys Pro His Gln Ser Ile Ala Ala Met Ala Glu Arg Tyr Gly Pro Leu
 50 55 60
 atg cac ctc cgc cta gga ttc gtg gac gtg gtt gtg gcc gcc tcc gcc 241
 Met His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala Ala Ser Ala
 65 70 75 80
 gcc gtg gcc gct cag ttc ttg aaa gtt cac gac tcg aac ttc tcc aac 289
 Ala Val Ala Ala Gln Phe Leu Lys Val His Asp Ser Asn Phe Ser Asn
 85 90 95
 cgg ccg ccg aac tcc ggc gcg gaa cac att gct tat aac tat caa gac 337

Arg	Pro	Pro	Asn	Ser	Gly	Ala	Glu	His	Ile	Ala	Tyr	Asn	Tyr	Gln	Asp		
			100					105					110				
ctc	gtc	ttc	gcg	ccc	tac	ggc	ccg	cgg	tgg	cgc	atg	ctt	agg	aag	atc	385	
Leu	Val	Phe	Ala	Pro	Tyr	Gly	Pro	Arg	Trp	Arg	Met	Leu	Arg	Lys	Ile		
		115					120					125					
acc	tcc	gtg	cat	ctc	ttc	tcg	gcc	aag	gcg	ttg	gat	gac	ttc	tgc	cat	433	
Thr	Ser	Val	His	Leu	Phe	Ser	Ala	Lys	Ala	Leu	Asp	Asp	Phe	Cys	His		
	130					135					140						
gtt	cgc	cag	gaa	gag	gtt	gca	act	ctg	aca	cgc	agt	cta	gca	agt	gca	481	
Val	Arg	Gln	Glu	Glu	Val	Ala	Thr	Leu	Thr	Arg	Ser	Leu	Ala	Ser	Ala		
145					150					155					160		
ggc	aaa	act	cca	gta	aaa	cta	ggg	cag	tta	cta	aac	gtg	tgc	acc	acg	529	
Gly	Lys	Thr	Pro	Val	Lys	Leu	Gly	Gln	Leu	Leu	Asn	Val	Cys	Thr	Thr		
			165					170						175			
aac	gcc	cta	gct	cgt	gta	atg	cta	ggg	cgg	aag	gtc	ttt	aat	gac	gga	577	
Asn	Ala	Leu	Ala	Arg	Val	Met	Leu	Gly	Arg	Lys	Val	Phe	Asn	Asp	Gly		
			180					185					190				
ggt	agc	aag	agc	gac	cca	aag	gcg	gag	gag	ttc	aag	tcg	atg	gtg	gag	625	
Gly	Ser	Lys	Ser	Asp	Pro	Lys	Ala	Glu	Glu	Phe	Lys	Ser	Met	Val	Glu		
		195					200					205					
gag	atg	atg	gtg	ttg	gcc	gga	agt	ttt	aac	atc	ggc	gat	ttc	att	ccg	673	
Glu	Met	Met	Val	Leu	Ala	Gly	Ser	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro		
	210					215					220						
gtc	ttg	ggt	tgg	ttt	gac	gtt	cag	ggt	atc	gta	ggg	aag	atg	aag	aaa	721	
Val	Leu	Gly	Trp	Phe	Asp	Val	Gln	Gly	Ile	Val	Gly	Lys	Met	Lys	Lys		
225					230					235					240		
cta	cac	gcg	cgt	ttt	gat	gcg	ttc	ttg	aac	acc	att	cta	gag	gaa	cac	769	
Leu	His	Ala	Arg	Phe	Asp	Ala	Phe	Leu	Asn	Thr	Ile	Leu	Glu	Glu	His		
				245					250					255			
aaa	tgt	gtc	aac	aat	caa	cac	acg	acg	ttg	tcg	aaa	gat	gtg	gac	ttc	817	
Lys	Cys	Val	Asn	Asn	Gln	His	Thr	Thr	Leu	Ser	Lys	Asp	Val	Asp	Phe		
			260					265					270				
ttg	agc	acc	cta	att	agg	ctc	aaa	gat	aat	ggg	gct	gat	atg	gat	tgt	865	
Leu	Ser	Thr	Leu	Ile	Arg	Leu	Lys	Asp	Asn	Gly	Ala	Asp	Met	Asp	Cys		
		275					280					285					
gaa	gag	gga	aaa	ctc	acc	gac	act	gaa	att	aag	gct	ttg	ctc	ttg	aac	913	
Glu	Glu	Gly	Lys	Leu	Thr	Asp	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn		
		290				295					300						
ctg	ttc	aca	gct	ggg	act	gat	aca	tca	tct	agc	act	gtg	gag	tgg	gca	961	
Leu	Phe	Thr	Ala	Gly	Thr	Asp	Thr	Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala		
305					310					315					320		
atc	gca	gaa	cta	cta	cgc	aac	cca	aaa	atc	tta	aac	caa	gca	caa	caa	1009	
Ile	Ala	Glu	Leu	Leu	Arg	Asn	Pro	Lys	Ile	Leu	Asn	Gln	Ala	Gln	Gln		
				325					330					335			
gag	ctt	gac	tta	gtg	gtg	ggt	caa	aat	cag	cta	gtc	aca	gaa	tct	gac	1057	

Glu	Leu	Asp	Leu	Val	Val	Gly	Gln	Asn	Gln	Leu	Val	Thr	Glu	Ser	Asp		
			340					345					350				
tta	acc	gat	cta	cct	ttc	ctg	caa	gca	ata	gtg	aag	gag	acc	ttc	agg	1105	
Leu	Thr	Asp	Leu	Pro	Phe	Leu	Gln	Ala	Ile	Val	Lys	Glu	Thr	Phe	Arg		
		355					360					365					
cta	cac	cca	tcc	acc	cca	ctc	tct	ctt	cca	aga	atg	gga	gct	cag	ggt	1153	
Leu	His	Pro	Ser	Thr	Pro	Leu	Ser	Leu	Pro	Arg	Met	Gly	Ala	Gln	Gly		
		370				375					380						
tgc	gag	atc	aat	ggc	tac	ttc	atc	ccc	aaa	ggc	gca	acg	ctt	ttg	gtc	1201	
Cys	Glu	Ile	Asn	Gly	Tyr	Phe	Ile	Pro	Lys	Gly	Ala	Thr	Leu	Leu	Val		
385					390					395					400		
aac	gtt	tgg	gcc	ata	gct	cgt	gat	ccc	aat	gtg	tgg	aca	aat	cct	ctt	1249	
Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp	Pro	Asn	Val	Trp	Thr	Asn	Pro	Leu		
			405					410						415			
gag	ttc	aac	cca	cac	cga	ttc	ttg	cct	ggg	gga	gaa	aag	ccc	aac	gtg	1297	
Glu	Phe	Asn	Pro	His	Arg	Phe	Leu	Pro	Gly	Gly	Glu	Lys	Pro	Asn	Val		
			420					425					430				
gat	att	aaa	ggg	aat	gac	ttt	gaa	gtg	att	cct	ttt	gga	gcc	ggg	cgt	1345	
Asp	Ile	Lys	Gly	Asn	Asp	Phe	Glu	Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg		
		435					440					445					
aga	ata	tgc	tct	ggg	atg	agt	ttg	ggg	ata	agg	atg	gtt	cac	ctg	ttg	1393	
Arg	Ile	Cys	Ser	Gly	Met	Ser	Leu	Gly	Ile	Arg	Met	Val	His	Leu	Leu		
		450				455					460						
gtt	gca	act	ttg	gtg	cat	gct	ttt	gat	tgg	gat	ttg	gtg	aat	gga	caa	1441	
Val	Ala	Thr	Leu	Val	His	Ala	Phe	Asp	Trp	Asp	Leu	Val	Asn	Gly	Gln		
					470				475						480		
tct	gta	gag	acg	ctc	aat	atg	gag	gaa	gct	tat	ggg	ctc	acc	ctt	caa	1489	
Ser	Val	Glu	Thr	Leu	Asn	Met	Glu	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln		
				485				490						495			
cga	gct	gtt	cct	ttg	atg	ttg	cat	cca	aag	ccc	aga	tta	caa	cca	cat	1537	
Arg	Ala	Val	Pro	Leu	Met	Leu	His	Pro	Lys	Pro	Arg	Leu	Gln	Pro	His		
			500					505					510				
ctc	tat	act	ctc	aat	taa	attgcaattt	gatttttgggtg	attataacaat								1585	
Leu	Tyr	Thr	Leu	Asn													
		515															
tataatcgag	ggacatagga	tccccattta	tttatattca	gttataagag	acttccaaca											1645	
aaggtctagc	tttcgacctt	aaaagttgta	aaagaggtcc	tacatatgta	aaagccccgcc											1705	
aaaggaaaac	tggttgtatt	caattccgct	aggccttgtc	cgaaagacct	catgaagact											1765	
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 <212> PRT

<400> 21

37

Arg Ile Cys Ser Gly Met Ser Leu Gly Ile Arg Met Val His Leu Leu
 450 455 460
 Val Ala Thr Leu Val His Ala Phe Asp Trp Asp Leu Val Asn Gly Gln
 465 470 475 480
 Ser Val Glu Thr Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln
 485 490 495
 Arg Ala Val Pro Leu Met Leu His Pro Lys Pro Arg Leu Gln Pro His
 500 505 510
 Leu Tyr Thr Leu Asn
 515

<210> 22
 <211> 1667
 <212> DNA
 <213> Gentian

<220>
 <221> CDS
 <222> (1)..(1431)

<400> 22
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 Pro Ile Leu Gly Asn Ile Pro His Leu Gly Ser Lys Pro His Gln Thr
 1 5 10 15
 ctc gcg gaa atg gcg aaa acc tac ggt ccg ctc atg cac ttg aag ttc 96
 Leu Ala Glu Met Ala Lys Thr Tyr Gly Pro Leu Met His Leu Lys Phe
 20 25 30
 ggg ctt aag gac gcg gtg gtg gcg tcg tct gcg tcg gtg gca gag cag 144
 Gly Leu Lys Asp Ala Val Val Ala Ser Ser Ala Ser Val Ala Glu Gln
 35 40 45
 ttt ctg aag aaa cac gac gtg aat ttc tcg aac cgg ccg cca aac tcc 192
 Phe Leu Lys Lys His Asp Val Asn Phe Ser Asn Arg Pro Pro Asn Ser
 50 55 60
 ggg gcc aaa cat ata gct tat aac tat cag gac ctg gta ttc gct ccc 240
 Gly Ala Lys His Ile Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro
 65 70 75 80
 tat gga ccc ccg tgg ccg ttg ctt agg aaa atc tgt tcc gtc cat ctt 288
 Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys Ile Cys Ser Val His Leu
 85 90 95
 ttc tcg tct aag gcc ttg gat gac ttt cag cat gtt cga cat gag gag 336
 Phe Ser Ser Lys Ala Leu Asp Asp Phe Gln His Val Arg His Glu Glu
 100 105 110
 ata tgc atc ctt ata cga gca ata gcg agt ggc ggt cat gct ccg gtg 384
 Ile Cys Ile Leu Ile Arg Ala Ile Ala Ser Gly Gly His Ala Pro Val
 115 120 125
 aat tta ggc aag tta tta gga gtg tgc aca acc aat gcc ctg gca aga 432
 Asn Leu Gly Lys Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg
 130 135 140
 gtg atg ctt gga aga aga gta ttc gaa ggc gac ggc ggc gag aat ccg 480

Val	Met	Leu	Gly	Arg	Arg	Val	Phe	Glu	Gly	Asp	Gly	Gly	Glu	Asn	Pro		
145					150					155					160		
cat	gcc	gac	gag	ttt	aaa	tca	atg	gtg	gtg	gag	att	atg	gtg	tta	gcc	528	
His	Ala	Asp	Glu	Phe	Lys	Ser	Met	Val	Val	Glu	Ile	Met	Val	Leu	Ala		
				165					170					175			
ggg	gca	ttc	aac	ttg	ggg	gat	ttc	atc	ccg	gtt	cta	gat	tg	ttc	gat	576	
Gly	Ala	Phe	Asn	Leu	Gly	Asp	Phe	Ile	Pro	Val	Leu	Asp	Trp	Phe	Asp		
			180					185					190				
ttg	caa	gga	att	gct	ggg	aaa	atg	aag	aaa	ctt	cat	gcc	cgt	ttc	gac	624	
Leu	Gln	Gly	Ile	Ala	Gly	Lys	Met	Lys	Lys	Leu	His	Ala	Arg	Phe	Asp		
			195				200					205					
aag	ttt	tta	aat	ggg	atc	cta	gaa	gat	cgt	aaa	tct	aac	ggc	tct	aat	672	
Lys	Phe	Leu	Asn	Gly	Ile	Leu	Glu	Asp	Arg	Lys	Ser	Asn	Gly	Ser	Asn		
	210					215					220						
gga	gct	gaa	caa	tac	gtg	gac	ttg	ctc	agt	gtg	ttg	atc	tct	ctt	caa	720	
Gly	Ala	Glu	Gln	Tyr	Val	Asp	Leu	Leu	Ser	Val	Leu	Ile	Ser	Leu	Gln		
225					230				235						240		
gat	agt	aat	atc	gac	ggg	ggg	gac	gaa	gga	acc	aaa	ctc	aca	gat	act	768	
Asp	Ser	Asn	Ile	Asp	Gly	Gly	Asp	Glu	Gly	Thr	Lys	Leu	Thr	Asp	Thr		
				245				250						255			
gaa	atc	aaa	gct	ctc	ctt	ttg	aac	ttg	ttc	ata	gcc	gga	aca	gac	act	816	
Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn	Leu	Phe	Ile	Ala	Gly	Thr	Asp	Thr		
			260					265					270				
tca	tca	agt	act	gta	gaa	tg	gcc	atg	gca	gaa	cta	atc	cga	aac	cca	864	
Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala	Met	Ala	Glu	Leu	Ile	Arg	Asn	Pro		
			275				280						285				
aag	tta	cta	gtc	caa	gcc	caa	gaa	gag	cta	gac	aga	gta	gtc	ggg	ccg	912	
Lys	Leu	Leu	Val	Gln	Ala	Gln	Glu	Glu	Leu	Asp	Arg	Val	Val	Gly	Pro		
	290					295					300						
aac	cga	ttc	gta	acc	gaa	tct	gat	ctt	cct	caa	ctg	aca	ttc	ctt	caa	960	
Asn	Arg	Phe	Val	Thr	Glu	Ser	Asp	Leu	Pro	Gln	Leu	Thr	Phe	Leu	Gln		
305					310					315					320		
gcc	gtc	atc	aaa	gag	act	ttc	agg	ctt	cat	cca	tcc	acc	cca	ctc	tct	1008	
Ala	Val	Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	Ser		
				325					330					335			
ctt	cca	cga	atg	gcg	gcg	gag	gac	tgt	gag	atc	aat	ggg	tat	tat	gtc	1056	
Leu	Pro	Arg	Met	Ala	Ala	Glu	Asp	Cys	Glu	Ile	Asn	Gly	Tyr	Tyr	Val		
			340					345					350				
tca	gaa	ggg	tcg	aca	ttg	ctc	gtc	aat	gtg	tg	gcc	ata	gct	cgt	gat	1104	
Ser	Glu	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp		
			355				360					365					
cca	aat	gcg	tg	gcc	aat	cca	cta	gat	ttc	aac	ccg	act	cgt	ttc	ttg	1152	
Pro	Asn	Ala	Trp	Ala	Asn	Pro	Leu	Asp	Phe	Asn	Pro	Thr	Arg	Phe	Leu		
	370					375					380						
gcc	ggg	gga	gag	aag	cct	aat	gtt	gat	gtt	aaa	ggg	aat	gat	ttt	gaa	1200	

Ala Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly Asn Asp Phe Glu	
385 390 395 400	
gtg ata cct ttc ggt gct ggg cgc agg ata tgt gcc gga atg agc tta	1248
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu	
405 410 415	
ggt ata cgg atg gtt caa cta gta acg gct tcg tta gtt cat tcg ttt	1296
Gly Ile Arg Met Val Gln Leu Val Thr Ala Ser Leu Val His Ser Phe	
420 425 430	
gat tgg gct ttg ttg gat gga ctt aaa ccc gag aag ctt gac atg gag	1344
Asp Trp Ala Leu Leu Asp Gly Leu Lys Pro Glu Lys Leu Asp Met Glu	
435 440 445	
gaa ggt tat gga cta acg ctt caa cga gct tca cct tta atc gtc cat	1392
Glu Gly Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His	
450 455 460	
cca aag ccg agg ctc tcg gct caa gtt tat tgt atg taa caagtttgtg	1441
Pro Lys Pro Arg Leu Ser Ala Gln Val Tyr Cys Met	
465 470 475	
aagccagtct gatttcagtt ggattttag ttattttatg atcatttggt attttatttt	1501
gtatttcggt tgaatacaat aaaggaagg tggatcgtct gctgtataat agcgacgttt	1561
taacgtgttg tgatagtacc gtgttttact aaaacgatgt cgtttgattt tttatagtat	1621
taaaaaaata aacagctgga ttttgaacca aaaaaaaaaa aaaaaa	1667

<210> 23
 <211> 476
 <212> PRT
 <213> Gentian

<400> 23	
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Leu Ala Glu Met Ala Lys Thr Tyr Gly Pro Leu Met His Leu Lys Phe	
20 25 30	
Gly Leu Lys Asp Ala Val Val Ala Ser Ser Ala Ser Val Ala Glu Gln	
35 40 45	
Phe Leu Lys Lys His Asp Val Asn Phe Ser Asn Arg Pro Pro Asn Ser	
50 55 60	
Gly Ala Lys His Ile Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro	
65 70 75 80	
Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys Ile Cys Ser Val His Leu	
85 90 95	
Phe Ser Ser Lys Ala Leu Asp Asp Phe Gln His Val Arg His Glu Glu	
100 105 110	
Ile Cys Ile Leu Ile Arg Ala Ile Ala Ser Gly Gly His Ala Pro Val	
115 120 125	
Asn Leu Gly Lys Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg	
130 135 140	
Val Met Leu Gly Arg Arg Val Phe Glu Gly Asp Gly Gly Glu Asn Pro	
145 150 155 160	
His Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala	

atg ctt gga agg agg gta ttc ggc gat ggg agc ggc ggc gta gat cct	145
Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro	
35 40 45	
cag gcg gac gag ttc aaa tcc atg gtg gtg gaa atc atg gtg ttg gcc	193
Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala	
50 55 60	
ggc gcg ttt aat cta ggt gat ttt att ccc gct ctt gat tgg ttc gat	241
Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe Asp	
65 70 75 80	
ctg cag gga att acg gca aaa atg aag aaa gtt cac gct cgt ttc gat	289
Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp	
85 90 95	
gcg ttc tta gac gcg atc ctt gag gag cac aaa tcc aac ggc tct cgc	337
Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg	
100 105 110	
gga gct aag caa cac gtt gac ttg ctg agt atg ttg atc tcc ctt caa	385
Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu Gln	
115 120 125	
gat aat aac att gat ggt gaa agt ggc gcc aaa ctc act gat aca gaa	433
Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr Glu	
130 135 140	
atc aaa gct ttg ctt ctg aac ttg ttc acg gct gga aca gac acg tca	481
Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser	
145 150 155 160	
tca agt act gtg gag tgg gca atc gca gag cta atc cga aac cca gaa	529
Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro Glu	
165 170 175	
gta ttg gtt caa gcc caa caa gag ctc gat aga gta gtt ggg cca agt	577
Val Leu Val Gln Ala Gln Gln Glu Leu Asp Arg Val Val Gly Pro Ser	
180 185 190	
cgt ctt gtg acc gaa tct gat ctg cct caa ttg gca ttc ctt caa gct	625
Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln Ala	
195 200 205	
gtc atc aaa gag act ttc aga ctt cat cca tcc act cca ctc tct ctt	673
Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu	
210 215 220	
cca cga atg gct tca gag ggt tgt gaa atc aat gga tac tcc atc cca	721
Pro Arg Met Ala Ser Glu Gly Cys Glu Ile Asn Gly Tyr Ser Ile Pro	
225 230 235 240	
aag ggt tcg aca ttg ctc gtt aac gta tgg tcc ata gcc cgt gat cct	769
Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ser Ile Ala Arg Asp Pro	
245 250 255	
agt ata tgg gcc gac cca tta gaa ttt agg ccg gca cgt ttc ttg ccc	817
Ser Ile Trp Ala Asp Pro Leu Glu Phe Arg Pro Ala Arg Phe Leu Pro	
260 265 270	

ggc gga gaa aag ccc aat gtt gat gtg aga ggc aat gat ttt gag gtc 865
 Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Val
 275 280 285
 ata cca ttt ggt gct gga cgt agg ata tgt gct gga atg agc ttg ggt 913
 Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly
 290 295 300
 tta aga atg gtt caa ctt tcg aca gct act ttg gtt cat tcg ttt aat 961
 Leu Arg Met Val Gln Leu Ser Thr Ala Thr Leu Val His Ser Phe Asn
 305 310 315 320
 tgg gat ttg ctg aat ggg atg agc cca gat aaa ctt gac atg gaa gaa 1009
 Trp Asp Leu Leu Asn Gly Met Ser Pro Asp Lys Leu Asp Met Glu Glu
 325 330 335
 gct tat ggg ctt aca ttg caa cgg gct tca cct ttg att gtc cac cca 1057
 Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His Pro
 340 345 350
 aag ccc agg ctt gct agc tct atg tat gtt aaa tga aattatgctg 1103
 Lys Pro Arg Leu Ala Ser Ser Met Tyr Val Lys
 355 360
 tgcgaataat tccttattta tagcaggaaa tgatcatcttg aattatgtgt aatgttcttc 1163
 taactttcga tggaagtgc aaacaagttt tattaaaaaa aaaaaaaaaa a 1214

<210> 25
 <211> 363
 <212> PRT
 <213> Lisianthus

<400> 25
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 Leu Gly Gln Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg Val
 20 25 30
 Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro
 35 40 45
 Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala
 50 55 60
 Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe Asp
 65 70 75 80
 Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp
 85 90 95
 Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg
 100 105 110
 Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu Gln
 115 120 125
 Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr Glu
 130 135 140
 Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser
 145 150 155 160
 Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro Glu
 165 170 175
 Val Leu Val Gln Ala Gln Gln Glu Leu Asp Arg Val Val Gly Pro Ser
 180 185 190
 Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln Ala

195	200	205
Val Ile Lys Glu Thr Phe Arg	Leu His Pro Ser Thr	Pro Leu Ser Leu
210	215	220
Pro Arg Met Ala Ser Glu Gly Cys Glu Ile Asn Gly Tyr Ser Ile Pro		
225	230	235
Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ser Ile Ala Arg Asp Pro		240
245	250	255
Ser Ile Trp Ala Asp Pro Leu Glu Phe Arg Pro Ala Arg Phe Leu Pro		
260	265	270
Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Val		
275	280	285
Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly		
290	295	300
Leu Arg Met Val Gln Leu Ser Thr Ala Thr Leu Val His Ser Phe Asn		
305	310	315
Trp Asp Leu Leu Asn Gly Met Ser Pro Asp Lys Leu Asp Met Glu Glu		
325	330	335
Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His Pro		
340	345	350
Lys Pro Arg Leu Ala Ser Ser Met Tyr Val Lys		
355	360	

<210> 26
 <211> 1757
 <212> DNA
 <213> Petunia sp.

<220>
 <221> CDS
 <222> (35)..(1525)

<400> 26
 ccgttgctgt cgagaaaaca gaaagaagag aaaa atg gac tac gtg aat att ttg 55
 Met Asp Tyr Val Asn Ile Leu
 1 5

ctg gga ctg ttt ttc act tgg ttc ttg gtg aat gga ctc atg tca ctt 103
 Leu Gly Leu Phe Phe Thr Trp Phe Leu Val Asn Gly Leu Met Ser Leu
 10 15 20

cga aga aga aaa atc tct aag aaa ctt cca cca ggt cca ttt cct ttg 151
 Arg Arg Arg Lys Ile Ser Lys Lys Leu Pro Pro Gly Pro Phe Pro Leu
 25 30 35

cct atc atc gga aat ctt cac tta ctt ggt aat cat cct cac aaa tca 199
 Pro Ile Ile Gly Asn Leu His Leu Leu Gly Asn His Pro His Lys Ser
 40 45 50 55

ctt gct caa ctt gca aaa att cat ggt cct att atg aat ctc aaa tta 247
 Leu Ala Gln Leu Ala Lys Ile His Gly Pro Ile Met Asn Leu Lys Leu
 60 65 70

ggc caa cta aac aca gtg gtc att tca tca tca gtc gtg gca aga gaa 295
 Gly Gln Leu Asn Thr Val Val Ile Ser Ser Ser Val Val Ala Arg Glu
 75 80 85

gtc ttg caa aaa caa gac tta aca ttt tcc aat agg ttt gtc ccg gac 343
 Val Leu Gln Lys Gln Asp Leu Thr Phe Ser Asn Arg Phe Val Pro Asp

90	95	100	
gta gtc cat gtc cga aat cac tcc gat ttt tct gtt gtt tgg tta cca Val Val His Val Arg Asn His Ser Asp Phe Ser Val Val Trp Leu Pro 105 110 115			391
gtc aat tct cga tgg aaa acg ctt cgc aaa atc atg aac tct agc atc Val Asn Ser Arg Trp Lys Thr Leu Arg Lys Ile Met Asn Ser Ser Ile 120 125 130 135			439
ttt tct ggt aac aag ctt gat ggt aat caa cat ctg agg tct aaa aag Phe Ser Gly Asn Lys Leu Asp Gly Asn Gln His Leu Arg Ser Lys Lys 140 145 150			487
gtc caa gag tta att gat tat tgt caa aag tgt gcc aag aat ggc gaa Val Gln Glu Leu Ile Asp Tyr Cys Gln Lys Cys Ala Lys Asn Gly Glu 155 160 165			535
gca gtg gat ata gga aga gca act ttt gga act act ttg aat ttg cta Ala Val Asp Ile Gly Arg Ala Thr Phe Gly Thr Thr Leu Asn Leu Leu 170 175 180			583
tcc aac acc att ttc tct aaa gat ttg act aat ccg ttt tct gat tct Ser Asn Thr Ile Phe Ser Lys Asp Leu Thr Asn Pro Phe Ser Asp Ser 185 190 195			631
gct aaa gag ttt aag gaa ttg gtt tgg aac att atg gtt gag gct gga Ala Lys Glu Phe Lys Glu Leu Val Trp Asn Ile Met Val Glu Ala Gly 200 205 210 215			679
aaa ccc aat ttg gtg gac tac ttt cct ttc ctt gag aaa att gat ccg Lys Pro Asn Leu Val Asp Tyr Phe Pro Phe Leu Glu Lys Ile Asp Pro 220 225 230			727
caa ggt ata aag cga cgc atg act aat aat ttt act aag ttt ctt ggc Gln Gly Ile Lys Arg Arg Met Thr Asn Asn Phe Thr Lys Phe Leu Gly 235 240 245			775
ctt atc agc ggt ttg att gat gac cgg tta aag gaa agg aat cta agg Leu Ile Ser Gly Leu Ile Asp Asp Arg Leu Lys Glu Arg Asn Leu Arg 250 255 260			823
gac aat gca aat att gat gtt tta gac gcc ctt ctc aac att agc caa Asp Asn Ala Asn Ile Asp Val Leu Asp Ala Leu Leu Asn Ile Ser Gln 265 270 275			871
gag aac cca gaa gag att gac agg aat caa atc gag cag ttg tgt ctg Glu Asn Pro Glu Glu Ile Asp Arg Asn Gln Ile Glu Gln Leu Cys Leu 280 285 290 295			919
gac ttg ttt gca gca ggg act gat act aca tcg aat acc ttg gag tgg Asp Leu Phe Ala Ala Gly Thr Asp Thr Thr Ser Asn Thr Leu Glu Trp 300 305 310			967
gca atg gca gaa cta ctt cag aat cca cac aca ttg cag aaa gca caa Ala Met Ala Glu Leu Leu Gln Asn Pro His Thr Leu Gln Lys Ala Gln 315 320 325			1015
gaa gaa ctt gca caa gtc att ggt aaa ggc aaa caa gta gaa gaa gca Glu Glu Leu Ala Gln Val Ile Gly Lys Gly Lys Gln Val Glu Glu Ala 1063			

330	335	340	
gat gtt gga cga cta cct tac ttg cga tgc ata gtg aaa gaa acc tta			1111
Asp Val Gly Arg Leu Pro Tyr Leu Arg Cys Ile Val Lys Glu Thr Leu			
345	350	355	
cga ata cac cca gcg gct cct ctc tta att cca cgt aaa gtg gag gaa			1159
Arg Ile His Pro Ala Ala Pro Leu Leu Ile Pro Arg Lys Val Glu Glu			
360	365	370	375
gac gtt gag ttg tct acc tat att att cca aag gat tca caa gtt cta			1207
Asp Val Glu Leu Ser Thr Tyr Ile Ile Pro Lys Asp Ser Gln Val Leu			
	380	385	390
gtg aac gta tgg gca att gga cgc aac tct gat cta tgg gaa aat cct			1255
Val Asn Val Trp Ala Ile Gly Arg Asn Ser Asp Leu Trp Glu Asn Pro			
	395	400	405
ttg gtc ttt aag cca gaa agg ttt tgg gag tca gaa ata gat atc cga			1303
Leu Val Phe Lys Pro Glu Arg Phe Trp Glu Ser Glu Ile Asp Ile Arg			
	410	415	420
ggt cga gat ttt gaa ctc att cca ttt ggt gct ggt cga aga att tgc			1351
Gly Arg Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys			
	425	430	435
cct gga ttg cct ttg gct atg agg atg att cca gta gca cta ggt tca			1399
Pro Gly Leu Pro Leu Ala Met Arg Met Ile Pro Val Ala Leu Gly Ser			
	440	445	450
ttg cta aac tca ttt aat tgg aaa cta tat ggt gga att gca cct aaa			1447
Leu Leu Asn Ser Phe Asn Trp Lys Leu Tyr Gly Gly Ile Ala Pro Lys			
	460	465	470
gat ttg gac atg cag gaa aag ttt ggc att acc ttg gcg aaa gcc caa			1495
Asp Leu Asp Met Gln Glu Lys Phe Gly Ile Thr Leu Ala Lys Ala Gln			
	475	480	485
cct ctg cta gct atc cca act ccc ctg tag ctatagggat aaattaagtt			1545
Pro Leu Leu Ala Ile Pro Thr Pro Leu			
	490	495	
gagggttttaa gttactagta gattctattg cagctatagg atttctttca ccatacagta 1605			
tgctttaccg ttggatgatg gaaagaaata tctatagctt tgggtttggt tagtttgcac 1665			
ataaaaaattg aatgaatgga ataccatgga gttataagaa ataataagac tatgattcct 1725			
accctacttg aacaatgaca tggctatttc ac 1757			

<210> 27

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

<400> 27
tttttttttt ttttttta

18

<210> 28
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 28
tttttttttt tttttttc

18

<210> 29
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 29
tttttttttt tttttttg

18

<210> 30
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<400> 30
Trp Ala Ile Gly Arg Asp Pro
1 5

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
<221> Modified Base
<222> (6)
<223> n is inosine

<220>
<221> Modified Base
<222> (9)
<223> n is inosine

<220>
<221> Modified Base
<222> (12)
<223> n is inosine

<220>
<221> Modified Base
<222> (15)
<223> n is inosine

<400> 31
tgggcnatng gnmngaycc

20

<210> 32
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<400> 32
Phe Arg Pro Glu Arg Phe
1 5

<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
<221> Modified base
<222> (11)
<223> n is inosine

<220>
<221> Modified base
<222> (14)
<223> n is inosine

<220>
<221> Modified base
<222> (20)
<223> n is inosine

<400> 33
aggaattymg nccngarmgn tt

22

<210> 34
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
<221> Modified base
<222> (3)
<223> n is inosine

<220>
<221> Modified base
<222> (9)
<223> n is inosine

<220>
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<220>
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<222> (15)
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<220>
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<220>
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<400> 34
ccnttyggng cnggnmgng natntgkscn gg

32

<210> 35
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<220>
<221> UNSURE
<222> (3)
<223> Xaa can be any amino acid.

<400> 35
Glu Phe Xaa Pro Glu Arg Phe
1 5

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
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<222> (3)
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<220>
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<223> n is inosine

<400> 36
ganttynnnc cnganmgntt

20

<210> 37
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 37
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28

<210> 38
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 38
gtcttggaca tcacacttca atctg

25

<210> 39
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 39
ccgaattccc cccccc

17

<210> 40
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
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<223> n is inosine

<220>
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<400> 40
 ccnggrcana tncyytncc ngcnccraan gg

32

<210> 41
 <211> 496
 <212> PRT
 <213> Petunia sp.

<400> 41

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Val	Asn	Gly	Leu	Met	Ser	Leu	Arg	Arg	Arg	Lys	Ile	Ser	Lys	Lys	Leu
		20						25					30		
Pro	Pro	Gly	Pro	Phe	Pro	Leu	Pro	Ile	Ile	Gly	Asn	Leu	His	Leu	Leu
		35					40					45			
Gly	Asn	His	Pro	His	Lys	Ser	Leu	Ala	Gln	Leu	Ala	Lys	Ile	His	Gly
	50					55					60				
Pro	Ile	Met	Asn	Leu	Lys	Leu	Gly	Gln	Leu	Asn	Thr	Val	Val	Ile	Ser
	65				70					75					80
Ser	Ser	Val	Val	Ala	Arg	Glu	Val	Leu	Gln	Lys	Gln	Asp	Leu	Thr	Phe
				85					90					95	
Ser	Asn	Arg	Phe	Val	Pro	Asp	Val	Val	His	Val	Arg	Asn	His	Ser	Asp
			100					105					110		
Phe	Ser	Val	Val	Trp	Leu	Pro	Val	Asn	Ser	Arg	Trp	Lys	Thr	Leu	Arg
		115					120					125			
Lys	Ile	Met	Asn	Ser	Ser	Ile	Phe	Ser	Gly	Asn	Lys	Leu	Asp	Gly	Asn
	130					135					140				
Gln	His	Leu	Arg	Ser	Lys	Lys	Val	Gln	Glu	Leu	Ile	Asp	Tyr	Cys	Gln
	145				150					155					160
Lys	Cys	Ala	Lys	Asn	Gly	Glu	Ala	Val	Asp	Ile	Gly	Arg	Ala	Thr	Phe
			165						170					175	
Gly	Thr	Thr	Leu	Asn	Leu	Leu	Ser	Asn	Thr	Ile	Phe	Ser	Lys	Asp	Leu
			180					185					190		
Thr	Asn	Pro	Phe	Ser	Asp	Ser	Ala	Lys	Glu	Phe	Lys	Glu	Leu	Val	Trp
		195					200					205			
Asn	Ile	Met	Val	Glu	Ala	Gly	Lys	Pro	Asn	Leu	Val	Asp	Tyr	Phe	Pro
	210					215					220				
Phe	Leu	Glu	Lys	Ile	Asp	Pro	Gln	Gly	Ile	Lys	Arg	Arg	Met	Thr	Asn
	225				230					235					240
Asn	Phe	Thr	Lys	Phe	Leu	Gly	Leu	Ile	Ser	Gly	Leu	Ile	Asp	Asp	Arg
			245						250					255	
Leu	Lys	Glu	Arg	Asn	Leu	Arg	Asp	Asn	Ala	Asn	Ile	Asp	Val	Leu	Asp
			260					265					270		
Ala	Leu	Leu	Asn	Ile	Ser	Gln	Glu	Asn	Pro	Glu	Glu	Ile	Asp	Arg	Asn
		275					280					285			
Gln	Ile	Glu	Gln	Leu	Cys	Leu	Asp	Leu	Phe	Ala	Ala	Gly	Thr	Asp	Thr
	290					295					300				
Thr	Ser	Asn	Thr	Leu	Glu	Trp	Ala	Met	Ala	Glu	Leu	Leu	Gln	Asn	Pro
	305				310					315					320
His	Thr	Leu	Gln	Lys	Ala	Gln	Glu	Glu	Leu	Ala	Gln	Val	Ile	Gly	Lys
			325						330					335	
Gly	Lys	Gln	Val	Glu	Glu	Ala	Asp	Val	Gly	Arg	Leu	Pro	Tyr	Leu	Arg

180					185					190						
Gly	Ala	Asp	Ala	Asp	His	Lys	Ala	Asp	Glu	Phe	Arg	Ser	Met	Val	Thr	
195					200					205						
Glu	Met	Met	Ala	Leu	Ala	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Val	Pro	
210					215					220						
Ser	Leu	Asp	Trp	Leu	Asp	Leu	Gln	Gly	Val	Ala	Gly	Lys	Met	Lys	Arg	
225					230					235					240	
Leu	His	Lys	Arg	Phe	Asp	Ala	Phe	Leu	Ser	Ser	Ile	Leu	Lys	Glu	His	
245					250					255						
Glu	Met	Asn	Gly	Gln	Asp	Gln	Lys	His	Thr	Asp	Met	Leu	Ser	Thr	Leu	
260					265					270						
Ile	Ser	Leu	Lys	Gly	Thr	Asp	Leu	Asp	Gly	Asp	Gly	Gly	Ser	Leu	Thr	
275					280					285						
Asp	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn	Met	Phe	Thr	Ala	Gly	Thr	
290					295					300						
Asp	Thr	Ser	Ala	Ser	Thr	Val	Asp	Trp	Ala	Ile	Ala	Glu	Leu	Ile	Arg	
305					310					315					320	
His	Pro	Asp	Ile	Met	Val	Lys	Ala	Gln	Glu	Glu	Leu	Asp	Ile	Val	Val	
325					330					335						
Gly	Arg	Asp	Arg	Pro	Val	Asn	Glu	Ser	Asp	Ile	Ala	Gln	Leu	Pro	Tyr	
340					345					350						
Leu	Gln	Ala	Val	Ile	Lys	Glu	Asn	Phe	Arg	Leu	His	Pro	Pro	Thr	Pro	
355					360					365						
Leu	Ser	Leu	Pro	His	Ile	Ala	Ser	Glu	Ser	Cys	Glu	Ile	Asn	Gly	Tyr	
370					375					380						
His	Ile	Pro	Lys	Gly	Ser	Thr	Leu	Leu	Thr	Asn	Ile	Trp	Ala	Ile	Ala	
385					390					395					400	
Arg	Asp	Pro	Asp	Gln	Trp	Ser	Asp	Pro	Leu	Ala	Phe	Lys	Pro	Glu	Arg	
405					410					415						
Phe	Leu	Pro	Gly	Gly	Glu	Lys	Ser	Gly	Val	Asp	Val	Lys	Gly	Ser	Asp	
420					425					430						
Phe	Glu	Leu	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Leu	
435					440					445						
Ser	Leu	Gly	Leu	Arg	Thr	Ile	Gln	Phe	Leu	Thr	Ala	Thr	Leu	Val	Gln	
450					455					460						
Gly	Phe	Asp	Trp	Glu	Leu	Ala	Gly	Gly	Val	Thr	Pro	Glu	Lys	Leu	Asn	
465					470					475					480	
Met	Glu	Glu	Ser	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Val	Pro	Leu	Val	
485					490					495						

Val His Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser
500 505 510

Gly

<210> 43
<211> 7
<212> PRT
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<400> 43
Arg Pro Pro Asn Ser Gly Ala
1 5

<210> 44
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<212> PRT
<213> Arabidopsis thaliana

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<221> UNSURE
<222> (8)
<223> Xaa can be any amino acid.

<220>
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<223> Xaa cab be any amino acid.

<220>
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<223> Xaa can be any amino acid.

<400> 44
Arg Pro Pro Asn Ser Gly Ala Xaa His Xaa Ala Tyr Asn Tyr Xaa Asp
1 5 10 15

Leu

<210> 45
<211> 521
<212> PRT
<213> Arabidopsis thaliana

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<222> (15)

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<220>

<221> UNSURE

<222> (18) .. (517)

<223> Xaa can be any amino acid. Positions 18-517
can be 0-500 amino acids.

<400> 45

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Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40					45			

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	50					55					60				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70					75					80

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		100						105						110	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		115					120					125			

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	130					135					140				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
145					150					155					160

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			165						170					175	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		180						185					190		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	195						200					205			

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	210					215					220				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
225					230					235					240

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			245						250					255	

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
260 265 270
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
275 280 285
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
290 295 300
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305 310 315 320
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325 330 335
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340 345 350
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355 360 365
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370 375 380
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385 390 395 400
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420 425 430
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465 470 475 480
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485 490 495
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500 505 510
Xaa Xaa Xaa Xaa Xaa Gly Gly Glu Lys
515 520